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-Tue Apr 17 15:46:22 2001

AD-6/23/1997
6/22/1998

us-09-446-543a-73.ra1

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2001, 15:39:49 ; Search time 61.54 Seconds

(without alignments)
6.868 Million cell updates/sec

Title: US-09-446-543a-73

Perfect score: 109

Sequence: 1 TPDINPARKYXXRGIRPVGKFX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.CONB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.CONB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.CONB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.CONB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUOS.CONB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	96.3	20	3	US-09-105-678A-46
2	105	96.3	21	3	US-09-105-678A-47
3	105	96.3	22	3	US-09-105-678A-48
4	105	96.3	31	3	US-09-105-678A-9
5	105	96.3	31	3	US-09-105-678A-43
6	105	96.3	32	3	US-09-105-678A-44
7	105	96.3	33	3	US-09-105-678A-45
8	104	95.4	20	3	US-09-105-678A-34
9	104	95.4	21	3	US-09-105-678A-35
10	104	95.4	21	3	US-09-105-678A-41
11	104	95.4	22	3	US-09-105-678A-36
12	104	95.4	22	3	US-09-105-678A-42
13	104	95.4	31	3	US-09-105-678A-7
14	104	95.4	31	3	US-09-105-678A-8
15	104	95.4	31	3	US-09-105-678A-31
16	104	95.4	31	3	US-09-105-678A-37
17	104	95.4	31	4	US-09-172-353-4
18	104	95.4	32	3	US-09-105-678A-32
19	104	95.4	32	3	US-09-105-678A-38
20	104	95.4	33	3	US-09-105-678A-33
21	104	95.4	33	3	US-09-105-678A-39
22	104	95.4	21	3	US-09-105-678A-28
23	103	89.9	19	3	US-09-105-678A-30
24	98	85.3	29	3	US-09-105-678A-29
25	44	40.4	349	1	US-08-118-270-71
26	44	40.4	349	5	PCR-US93-08528-71
27	44	40.4	349	5	Sequence 71, Appl

28	41	37.6	547	1	US-08-083-948-8	Sequence 8, Appl
29	41	37.6	547	1	US-08-393-785-8	Sequence 8, Appl
30	41	37.6	547	1	US-08-475-694-8	Sequence 8, Appl
31	41	37.6	547	1	US-08-712-057-8	Sequence 8, Appl
32	39	35.8	162	4	US-08-992-176-9	Sequence 9, Appl
33	39	35.8	555	2	US-08-982-232-7	Sequence 9, Appl
34	39	35.8	555	2	US-08-982-232-14	Sequence 14, Appl
35	38.5	35.3	555	2	US-08-453-702A-98	Sequence 98, Appl
36	38.5	35.3	831	1	US-08-073-384C-5	Sequence 5, Appl
37	38.5	35.3	831	1	US-08-254-359A-5	Sequence 5, Appl
38	38.5	35.3	831	1	US-08-483-043-5	Sequence 5, Appl
39	38.5	35.3	831	1	US-08-481-238-5	Sequence 5, Appl
40	38.5	35.3	831	2	US-08-471-066B-5	Sequence 5, Appl
41	38.5	35.3	831	2	US-08-484-956-5	Sequence 5, Appl
42	38.5	35.3	831	2	US-08-757-653-5	Sequence 5, Appl
43	38.5	35.3	831	2	US-08-599-491-5	Sequence 5, Appl
44	38.5	35.3	831	2	US-08-756-386-5	Sequence 5, Appl
45	38.5	35.3	831	2	US-08-823-516-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-105-678A-46

Sequence 46, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takao

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 122118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-678A-46

Query Match

Best Local Similarity 96.3%

Score 105, DB 3, Length 20,

Pred. No. 1, 5e-11;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXRGIRPVGRF 20
|||||||
DB 1 TPDINPAMYASRGIRPVGRF 20

RESULT 2

US-09-105-678A-47
Sequence 47, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-47

Query Match 96.3%; Score 105; DB 3; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.5e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXRGIRPVGRF 20
|||||||
DB 1 TPDINPAMYASRGIRPVGRF 20

RESULT 3
US-09-105-678A-48
Sequence 48, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-48

Query Match 96.3%; Score 105; DB 3; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.6e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXRGIRPVGRF 20
|||||||
DB 1 TPDINPAMYASRGIRPVGRF 20

RESULT 4
US-09-105-678A-9
Sequence 9, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.

REGISTRATION NUMBER: 27, 026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-9

Query Match 96.3%; Score 105; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAWYXXRGIRPVGR 20
|||||
Db 12 TPDINPAWYASRGIRPVGR 31

RESULT 5
US-09-105-678A-43
Sequence 43, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
DEPARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIDR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27, 026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-43

Query Match 96.3%; Score 105; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAWYXXRGIRPVGR 20
|||||
Db 12 TPDINPAWYASRGIRPVGR 31

RESULT 6
US-09-105-678A-44
Sequence 44, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
DEPARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIDR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27, 026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-44

Query Match 96.3%; Score 105; DB 3; Length 32;
Best Local Similarity 90.0%; Pred. No. 2.5e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAWYXXRGIRPVGR 20
|||||
Db 12 TPDINPAWYASRGIRPVGR 31

RESULT 7
US-09-105-678A-45
Sequence 45, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-45

Query Match 96.3%; Score 105; DB 3; Length 33;
Best Local Similarity 90.0%; Pred. No. 2.2e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TPDINPAMYXXRGIRPVGRF 20
||||||| |||||||
Db 12 TPDINPAMYASRGIRPVGRF 31

RESULT 8
US-09-105-678A-34
Sequence 34, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-34

Query Match 95.4%; Score 104; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TPDINPAMYXXRGIRPVGRF 20
||||||| |||||||
Db 1 TPDINPAMYAGIRPVGRF 20

RESULT 9
US-09-105-678A-40
Sequence 40, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-40

Query Match 95.4%; Score 104; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e-11;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
Db 1 TPDINPAMYTGRCIRPVGRF 20

RESULT 10

US-09-105-678A-35
Sequence 35, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-678A-35

Query Match 95.4%; Score 104; DB 3; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e-11;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
Db 1 TPDINPAMYTGRCIRPVGRF 20

RESULT 11

US-09-105-678A-41

Sequence 41, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-678A-41

Query Match 95.4%; Score 104; DB 3; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e-11;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
Db 1 TPDINPAMYTGRCIRPVGRF 20

RESULT 12

US-09-105-678A-36

Sequence 36, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-36

Query Match 95.4%; Score 104; DB 3; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
|||||
DB 1 TPDINPAMYAGRGIRPVGRF 20

RESULT 13
US-09-105-678A-42
Sequence 42, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-42

Query Match 95.4%; Score 104; DB 3; Length 22;

Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
|||||
DB 1 TPDINPAMYAGRGIRPVGRF 20

RESULT 14
US-09-105-678A-7
Sequence 7, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-7

Query Match 95.4%; Score 104; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 3.5e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDINPAMYXXRGIRPVGRF 20
|||||
DB 12 TPDINPAMYAGRGIRPVGRF 31

RESULT 15
US-09-105-678A-8
Sequence 8, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND


```

: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/105.678A
: FILING DATE: 26-JUN-1998
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: JP 172118/1997
: FILING DATE: 27-JUN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Conlin, David G.
: REGISTRATION NUMBER: 27,026
: REFERENCE/DOCKET NUMBER: 48466-342
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 31 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-105-678A-B

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Query Match          95.4%; Score 104; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. NO.3.5e-11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 TPDINPAMYXXRGIRPVGRF 20
   ||||||| |||||||
DB 12 TPDINPAMVTGIRPVGRF 31

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Search completed: April 17, 2001, 15:39:49
 Job time: 318 sec

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us-09-446-543a-73.rag

1-15 African

137
Page 1

DM protein - protein search, using sw model

Title: US-09-446-543A-73

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perfect score: 109
sequence:      1 TPDINPAWYXXRGIRPVGRFX 22
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Scoring table: BLOSUM62

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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2:	/SIDS1/gcgdata/gemseq/gemseqp/AA1981.DAT *
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13:	/SIDS1/gcgdata/gemseq/gemseqp/AA1992.DAT *
14:	/SIDS1/gcgdata/gemseq/gemseqp/AA1993.DAT *
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19:	/SIDS1/gcgdata/gemseq/gemseqp/AA1998.DAT *
20:	/SIDS1/gcgdata/gemseq/gemseqp/AA1999.DAT *
21:	/SIDS1/gcgdata/gemseq/gemseqp/AA2000.DAT *
22:	/SIDS1/gcgdata/gemseq/gemseqp/AA2001.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	105	96.3	20	18	W31394	Human type G prote
2	105	96.3	20	20	W87226	Human type I ligand
3	105	96.3	20	21	B10365	Human type G prote
4	105	96.3	20	21	Y49294	Human type G prote
5	105	96.3	21	18	W31395	Human type G prote
6	105	96.3	21	21	B10366	Human type G prote
7	105	96.3	22	18	W31396	Human type G prote
8	105	96.3	22	21	B10367	Human type G prote
9	105	96.3	31	18	W31391	Human type I ligand
10	105	96.3	31	20	W87235	Human type I ligand
11	105	96.3	31	20	W87615	Human type I ligand

[illegible]

XX Ligand peptide for G protein-coupled receptor - acts by modulating
 PT function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2: Page 185; 258pp: English.

CC This sequence represents a peptide fragment from a novel human type
 CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the
 CC sequence represented in W31390 and is used in an assay to monitor ligand
 CC binding to the G protein-coupled receptor protein. Pharmaceutical
 CC compositions containing this ligand may be used as a pituitary function
 CC modulator, a central nervous system modulator or a pancreatic function
 CC modulator. This ligand could have specific applications as a prophylactic
 CC or therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidemia,
 CC hypercholesterolemia, hyperglycemia, hypoparathyroidism, diabetes,
 CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
 CC rheumatoid arthritis, spinal injury, transient brain ischemia, epilepsy,
 CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 CC osteoporosis and/or oligosaccharia. Assays can also be developed to screen
 CC compounds which are capable of altering the binding activity of the
 CC ligand affecting activation of the G protein-coupled receptor protein.
 CC
 SQ Sequence 20 AA:

Query Match 96.3%; Score 105; DB 18; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.3e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPVGRF 20
 |||||
 DB 1 tpdinpwasyrgirpvgrrf 20

RESULT 2
 W97236
 ID W97236 standard; peptide: 20 AA.
 XX

AC W97236;
 XX

DT 06-MAY-1999 (first entry)
 XX

DE Human type ligand polypeptide fragment.
 XX

XX Rat type ligand; modulation; prolactin secretion;
 KW G protein-coupled receptor; GPCR; hypovarianism; gonocyst cacosgenesis;
 KW menopausal syndrome; euthyroid; hypometabolism; lactation;
 KW pituitary adenomatosis; brain tumour; emmenopathy; autolimmune disease;
 KW prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
 KW acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome;
 KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
 KW contraceptive; placental function; chorioncarcinoma; hydatid mole;
 KW interruption mole; abortion; unfertility fetus; abnormal saccharometabolism;
 KW abnormal lipidmetabolism; oxytocia.
 XX

OS Homo sapiens.
 XX

PM W09858962-A1.
 XX

PD 30-DEC-1998.
 XX

PF 22-JUN-1998; 98WO-JP02765.
 XX

PR 23-JUN-1997; 97JP-0165437.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PT Fujii R, Hinuma S, Kawamata Y, Matsumoto H;
 XX

DR WPI; 1999-105614/09.

XX Use of G protein-coupled receptor ligands - for modulating prolactin
 PT secretion or placental function, e.g. for treating menopausal
 PT syndrome, tumours, autoimmune disease or abnormal pregnancy
 XX
 PS Claim 3: Page 166; 241pp: English.

CC The present sequence represents a human type ligand fragment. It
 CC is used in the course of the invention. The specification describes
 CC an agent for modulating prolactin secretion which comprises a
 CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
 CC protein. The agents for promoting prolactin secretion can be used for
 CC treating or preventing hypovarianism, gonocyst cacosgenesis, menopausal
 CC syndrome, euthyroid or hypometabolism. They can be used for promoting
 CC lactation in a domestic mammal and as an aphrodisiac. The agents for
 CC inhibiting prolactin secretion can be used for treating or preventing
 CC pituitary adenomatosis, brain tumour, emmenopathy, autolimmune disease,
 CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
 CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome,
 CC Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
 CC The inhibitory agents can also be used as contraceptives. The agents for
 CC modulating placental function can be used for treating or preventing
 CC chorioncarcinoma, hydatid mole, interruption mole, unfertility fetus,
 CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
 CC
 SQ Sequence 20 AA:

Query Match 96.3%; Score 105; DB 20; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.3e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPVGRF 20
 |||||
 DB 1 tpdinpwasyrgirpvgrrf 20

RESULT 3
 B10365
 ID B10365 standard; peptide: 20 AA.
 XX

AC B10365;
 XX

DT 24-NOV-2000 (first entry)
 XX

DE Human oxytocin secretion promoting peptide SEQ ID NO: 35.
 XX

XX Human; oxytocin secretion promoter; G protein-coupled receptor protein;
 KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KW caesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.
 XX

OS Homo sapiens.
 XX

PM W0200038704-A1.
 XX

PD 06-JUL-2000.
 XX

PF 22-DEC-1999; 99WO-JP07199.
 XX

PR 25-DEC-1998; 98JP-0369585.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PT Matsumoto H, Kitada C, Hinuma S;
 XX

DR WPI; 2000-452298/39.
 XX

PT Physiologically-active polypeptide recognized as ligand by G
 PT protein-coupled receptor protein, for promoting secretion of oxytocin,
 PT as drugs for diseases relating to oxytocin secretion and in veterinary
 PT medicine
 XX

Query Match 96.3%; Score 105; DB 18; Length 21;
 Best Local Similarity 90.0%; Pred. No. 1.4e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAWYXXRGIRPVGRF 20
 |||||
 Db 1 tpdinpawyasrgirpvgrf 20

RESULT 6

B10366 B10366 standard; peptide: 21 AA.

AC 810366;

DT 24-NOV-2000 (first entry)

DE Human oxytocin secretion promoting peptide SEQ ID NO: 36.

XX Human; oxytocin secretion promoter; G protein-coupled receptor protein;
 KM treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KM caesarean section; artificial fertilization; galactostasis; goat; pig;
 KM veterinary medicine; milk production.

XX Homo sapiens.

PN WO200038704-A1.

XX 06-JUL-2000.

PF 22-DEC-1999; 99WO-JP07199.

XX 25-DEC-1998; 98JP-0369585.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Matsumoto H, Kitada C, Hinuma S;

DR WPI; 2000-452298/39.

XX Physiologically-active polypeptide recognized as ligand by G
 PT protein-coupled receptor protein, for promoting secretion of oxytocin,
 PT as drugs for diseases relating to oxytocin secretion and in veterinary
 PT medicine -
 XX
 PS Disclosure; Page 63; 72pp; Japanese.

CC This invention describes a novel oxytocin secretion-regulating agent
 CC which contains a ligand peptide or its salt for the G protein-coupled
 CC receptor protein. It is useful in the form of drugs for ameliorating,
 CC preventing and treating diseases relating to oxytocin secretion e.g.,
 CC weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a human peptide which acts as an oxytocin secretion
 CC promoter.

XX Sequence 21 AA:

Query Match 96.3%; Score 105; DB 21; Length 21;
 Best Local Similarity 90.0%; Pred. No. 1.4e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAWYXXRGIRPVGRF 20
 |||||
 Db 1 tpdinpawyasrgirpvgrf 20

RESULT 7
 B10367 B10367 standard; peptide: 21 AA.

ID W31396 standard; Peptide: 22 AA.

XX W31396;

AC 06-APR-1998 (first entry)

XX Human type G protein-coupled receptor ligand fragment 6.

DE G protein-coupled receptor; ligand binding; pharmaceutical;
 KM modulator; pituitary; central nervous system; pancreas; prophylactic;
 KM therapeutic agent.

XX Homo sapiens.

PN WO9724436-A2.

XX 10-JUL-1997.

PF 26-DEC-1996; 96WO-JP03821.

XX 18-SEP-1996; 96JP-0246573.

PR 28-DEC-1995; 95JP-0343371.

PR 15-MAR-1996; 96JP-0059419.

PR 12-ADG-1996; 96JP-0211805.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;

PI Kawamata Y, Kitada C;

DR WPI; 1997-363672/33.

DR N-PSDB; V02433.

XX Claim 2; Page 186; 258pp; English.

XX This sequence represents a peptide fragment from a novel human type
 CC ligand polypeptide corresponding to amino acid residues 34 to 55 of the
 CC sequence represented in W31390 and is used in an assay to monitor ligand
 CC binding to the G protein-coupled receptor protein. Pharmaceutical
 CC compositions containing this ligand may be used as a pituitary function
 CC modulator, a central nervous system modulator or a pancreatic function
 CC modulator. This ligand could have specific applications as a prophylactic
 CC or therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and hypothyroidism, hyperlipidaemia,
 CC hypercholesterolaemia, hyperglycaemia, hyperprolactinaemia, diabetes,
 CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
 CC rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy,
 CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis and/or oligosaccharia. Assays can also be developed to screen
 CC compounds which are capable of altering the binding activity of the
 CC ligand affecting activation of the G protein-coupled receptor protein.

XX Sequence 22 AA:

Query Match 96.3%; Score 105; DB 18; Length 22;
 Best Local Similarity 90.0%; Pred. No. 1.5e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAWYXXRGIRPVGRF 20
 |||||
 Db 1 tpdinpawyasrgirpvgrf 20

RESULT 8
 B10367 B10367 standard; peptide: 22 AA.

XX OS Homo sapiens.
 XX XX WO200038704-A1.
 XX PN 06-JUL-2000.
 XX PD
 XX PF 22-DEC-1999; 99WO-JP07199.
 XX XX 25-DEC-1999; 98JP-0369585.
 XX PR
 XX XX (TAKE) TAKEDA CHEM IND LTD.
 XX PA Matsumoto H, Kitada C, Hinuma S;
 XX PI WPI: 2000-452298/39.
 XX DR
 XX PT Physiologically-active polypeptide recognized as ligand by G
 XX PT protein-coupled receptor protein, for promoting secretion of oxytocin,
 XX PT as drugs for diseases relating to oxytocin secretion and in veterinary
 XX PT medicine -
 XX PS Disclosure: Page 62; 72pp; Japanese.
 XX CC This invention describes a novel oxytocin secretion-regulating agent
 XX CC which contains a ligand peptide or its salt for the G protein-coupled
 XX CC receptor protein. It is useful in the form of drugs for ameliorating,
 XX CC preventing and treating diseases relating to oxytocin secretion e.g.,
 XX CC wear pains and atonic bleeding, before and after expulsion of placenta,
 XX CC uterine recovery failure, caesarean section, stoppage of artificial
 XX CC fertilization or galactostasis and is also applicable in veterinary
 XX CC medicine for promoting milk production in cow, goat and pig. This
 XX CC sequence represents a human peptide which acts as an oxytocin secretion
 XX CC promoter.
 XX SO Sequence 31 AA;

Query Match 96.3%; Score 105; DB 21; Length 31;
 Best Local Similarity 90.0%; Pred. No. 2.1e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPVGRF 20
 |||||
 Db 12 tpdinpawysrgirpvrgrf 31

RESULT 13
 RESULF 13
 ID Y49291 standard; peptide: 31 AA.
 XX Y49291;
 AC Y49291;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 XX 19P2 ligand peptide fragment.
 DE
 XX Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
 KM pituitary; regulatory mechanism; central nervous system; pancreatic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 31 /note="C-terminal amide"
 FT
 XX WO9960112-A1.
 XX PN 25-NOV-1999.
 XX PD 20-MAY-1999; 99WO-JP02650.
 XX PF 21-MAY-1998; 98JP-0140293.
 XX PR

XX XX (TAKE) TAKEDA CHEM IND LTD.
 XX PA Matsumoto H, Kitada C, Hinuma S;
 XX PI WPI: 2000-039381/03.
 XX DR
 XX PT New monoclonal antibodies, useful in diagnosis, as drugs and in
 XX PT studying diseases related to ligand abnormality -
 XX PS Disclosure: Page 26; 73pp; Japanese.
 XX CC The invention provides a monoclonal antibody which has a specific
 XX CC reaction with the part peptide of the C-terminal of 19P2 ligand or its
 XX CC derivative. The antibodies can be used in diagnosis or to treat or
 XX CC prevent diseases associated with abnormality in the pituitary function
 XX CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 XX CC nervous regulatory mechanism, and pancreatic function regulatory
 XX CC mechanism. The antibody-based immunoassay can also be applied in
 XX CC clarifying the physiological functions of the ligand and its derivative.
 XX CC Sequences Y49290-302 represent peptide fragments of the 19P2 ligand.
 XX SO Sequence 31 AA;

Query Match 96.3%; Score 105; DB 21; Length 31;
 Best Local Similarity 90.0%; Pred. No. 2.1e-11;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPVGRF 20
 |||||
 Db 12 tpdinpawysrgirpvrgrf 31

RESULT 14
 W31392
 ID W31392 standard; peptide: 32 AA.
 XX W31392;
 AC
 XX DT 06-APR-1998 (first entry)
 XX
 XX Human type G protein-coupled receptor ligand fragment 2.
 DE
 XX G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 OS Homo sapiens.
 XX
 XX WO9724436-A2.
 XX PN 10-JUL-1997.
 XX PD 26-DEC-1996; 96WO-JP03821.
 XX PF 18-SEP-1996; 96JP-0246573.
 XX PR 28-DEC-1995; 95JP-0343371.
 XX PR 15-MAR-1996; 96JP-0059419.
 XX PR 12-AUG-1996; 96JP-0211805.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX XX Fuji R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 XX PI Kawamata Y, Kitada C;
 XX DR WPI: 1997-363672/33.
 XX DR N-PSDB; V02429.
 XX PT Ligand peptide for G protein-coupled receptor - acts by modulating
 XX PT function in the central nervous system, pancreas and pituitary gland
 XX PS Claim 2; Page 185; 258pp; English.

XX This sequence represents a peptide fragment from a novel human type
 CC ligand polypeptide corresponding to amino acid residues 23 to 54 of the
 CC sequence represented in W31390 and is used in an assay to monitor ligand
 CC binding to the G protein-coupled receptor protein. Pharmaceutical
 CC compositions containing this ligand may be used as a pituitary function
 CC modulator, a central nervous system modulator or a pancreatic function
 CC modulator. This ligand could have specific applications as a prophylactic
 CC or therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidemia,
 CC hypercholesterolemia, hyperglycaemia, hyperprolactinaemia, diabetes,
 CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
 CC rheumatoid arthritis, spinal injury, transient brain ischemia, epilepsy,
 CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis and/or oligosaccharia. Assays can also be developed to screen
 CC compounds which are capable of altering the binding activity of the
 CC ligand affecting activation of the G protein-coupled receptor protein.

SO Sequence 32 AA;

Query Match

Best Local Similarity 96.3%; Score 105; DB 18; Length 32;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPYGRF 20

DB 12 tpdinpawyasrglrpygrf 31

RESULT 15

ID B10363 standard; peptide: 32 AA.

XX B10363;

DT 24-NOV-2000 (first entry)

DE Human oxytocin secretion promoting peptide SEQ ID NO: 33.

XX Human: oxytocin secretion promoter; G protein-coupled receptor protein;

KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;

KW caesarean section; artificial fertilization; galactostasis; goat; pig;

XX veterinary medicine; milk production.

XX Homo sapiens.

XX WO200038704-A1.

XX 06-JUL-2000.

XX 22-DEC-1999; 99WO-9P07199.

XX 25-DEC-1998; 98JP-0369585.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsuoto H, Kitada C, Hinuma S;

XX WPI; 2000-452298/39.

XX Physiologically-active polypeptide recognized as ligand by G

XX protein-coupled receptor protein, for promoting secretion of oxytocin,

XX as drugs for diseases relating to oxytocin secretion and in veterinary

XX medicine

XX Disclosure; Page 62; 72pp; Japanese.

CC preventing and treating diseases relating to oxytocin secretion e.g.
 CC weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a human peptide which acts as an oxytocin secretion
 CC promoter.

SO Sequence 32 AA;

Query Match

Best Local Similarity 96.3%; Score 105; DB 21; Length 32;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRPYGRF 20

DB 12 tpdinpawyasrglrpygrf 31

Search completed: April 17, 2001, 15:38:42
 Job time: 349 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 17, 2001, 15:45:59 ; Search time 70.08 seconds
(without alignments)
21.574 Million cell updates/sec

Title: US-09-446-543a-73

Perfect score: 109

Sequence: 1 TPDINPAWYXXRGIRPVGRFX 22

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.5	45.4	664	2 F83376	conserved hypothet
2	49.5	45.0	790	2 T47959	hypothetical prote
3	46	42.2	333	2 H82852	hydroxybenzoate oc
4	45	41.3	767	2 T21969	hypothetical prote
5	44	40.4	250	2 G83400	hypothetical prote
6	44	40.4	284	2 F71015	hypothetical prote
7	43.5	39.9	1501	2 T45623	hypothetical prote
8	43	38.4	220	2 C83292	probable glutathio
9	43	38.4	232	2 G75608	hypothetical prote
10	43	39.4	309	2 T32376	hypothetical prote
11	43	39.4	376	2 A48197	opsin, ocellar - A
12	43	39.4	376	2 B48197	opsin, lateral eye
13	43	39.4	476	2 G64720	probable amino aci
14	43	38.4	719	2 S61046	ARPI protein - yea
15	43	38.4	1296	2 T16859	hypothetical prote
16	42.5	38.0	443	2 T21499	pyruvate dehydroge
17	42	38.5	428	2 F81694	N-acetylglutamate
18	41.5	38.1	345	2 D84012	hypothetical prote
19	41	37.6	128	2 S76955	hypothetical prote
20	41	37.6	284	2 A75117	hypothetical prote
21	41	37.6	338	2 T20100	hypothetical prote
22	41	37.6	342	2 B64395	malic acid transpo
23	41	37.6	343	2 T46534	malic acid transpo
24	41	37.6	347	2 H64371	malic acid transpo
25	41	37.6	986	1 OYUGA	speract receptor p
26	41	37.6	2155	2 T30197	alpha tectorin - m
27	40.5	37.2	779	2 T48717	related to BCS1 pr
28	40.5	37.2	1540	2 T45619	hypothetical prote
29	40	36.7	184	2 T35841	probable membrane

30	40	36.7	324	2 T35901	probable arae fam1
31	40	36.7	329	2 H70744	hypothetical prote
32	40	36.7	341	2 T35426	probable oxidoredu
33	40	36.7	359	2 T40084	PMP domain protel
34	40	36.7	390	2 G82844	cysteine synthase
35	40	36.7	430	1 B65009	conserved hypothet
36	40	36.7	462	2 T00708	violaxanthin de-ep
37	40	36.7	468	2 C83160	nitrite extrusion
38	40	36.7	546	2 A32260	cholesterol oxidas
39	40	36.7	581	2 A42743	pol polyprotein -
40	40	36.7	843	1 GNVK	pol polyprotein -
41	40	36.7	1196	1 GNMVGV	pol polyprotein -
42	40	36.7	1196	1 GNMVGV	pol polyprotein -
43	40	36.7	1762	2 T03222	probable polyketid
44	40	36.7	2100	2 T03223	probable polyketid
45	40	36.7	7962	2 I38346	elastic titin - hu

ALIGNMENTS

RESULT 1
F83376
conserved hypothetical protein PA2151 [Imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83376
R:Stover, C.K.; Pham, X.Q.; Ewlin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: F83376
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-664 <STO>
A:Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AA05539.1; GSPDB:GN
C:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2151

Query Match 45.4%; Score 49.5; DB 2; Length 664;
Best Local Similarity 62.5%; Pred. No. 2.6;
Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

OY 1 TPDINPAWYXXRGIRP 16
||||| : | | |
DB 478 TPDINP-WFLQNSGRP 492

RESULT 2
T47959
hypothetical protein F15G16.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47959
R:De Haan, M.; Maarse, A.C.; Griwell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; O
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z24480
A:Accession: T47959
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-790 <DEH>
A:Cross-references: EMBL:AL132959
A:Experimental source: cultivar Columbia; BAC clone F15G16
C:Genetics:
A:Map position: 3
A:introns: 39/1; 678/2; 698/3; 773/2
A:Note: F15G16.60

Query Match 45.0% Score 49; DB 2; Length 790;

Best local Similarity 47.4%; Pred. No. 3.7;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 PDINPAMXXRGIRPVGR 20

DB 366 PPHNPRTYSGRGLQPHGRW 384

RESULT 3

H82852 hydroxybenzoate octaprenyltransferase XE0068 [Imported] - xylella fastidiosa (strain 9a5

C:Species: xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Accession: H82852

R:Anonymous, The xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen xylella fastidiosa.

A:Reference number: A82515; MID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82852

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <SIM>

A:Cross-references: GB:AE003860; GB:AE003849; MID:99104830; PIDN:AAF82881.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.N.; Camargo, L.E.A.; Carrato, D.M.; Carier, H

de Melo, E.; Docena, C.; El-Dorri, M.; Facincanli, A.P.; Ferreira, A.J.S.

submitted to: Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

chedo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Rodrigues, V.; Rosa, A.C.R.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XE0068

C:Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 42.2% Score 46; DB 2; Length 333;

Best local Similarity 53.3%; Pred. No. 4.9;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 INPAMXXRGIRPVG 18

DB 54 LDPTWKLARDRVRG 68

RESULT 4

T21969 hypothetical protein F38E11.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21969

R:Matthews, P.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19495

A:Accession: T21969

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-767 <SIM>

A:Cross-references: PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11.7

A:Experimental source: clone F38E11

C:Genetics:

A:Gene: CESP:F38E11.7

A:Map position: 4

A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 6

Query Match 41.3% Score 45; DB 2; Length 767;

Best local Similarity 73.0%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDINPAM 9

DB 747 PDVKKPAM 754

RESULT 5

G83400 hypothetical protein PA1952 [Imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83400

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MID:20437337

A:Accession: G83400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: GB:AE004622; GB:AE004091; MID:99947948; PIDN:AA605340.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1952

Query Match 40.4% Score 44; DB 2; Length 250;

Best local Similarity 47.1%; Pred. No. 7.8;

Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 PDINPAMXXRGIRPVG 18

DB 233 PALNCAMEDQRLALRPSG 249

RESULT 6

F71015 hypothetical protein PH1420 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C:Accession: F71015

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; MID:98344137

A:Accession: F71015

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-284 <KAW>

A:Cross-references: GB:AP000006; MID:93236133; PIDN:BA30526.1; PID:93257843

A:Note: This accession replaces an interim accession for a sequence replaced by Genba

C:Genetics:

A:Gene: PH1420

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1420

Query Match 40.4% Score 44; DB 2; Length 284;

Best local Similarity 44.4%; Pred. No. 8.9;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 PDINPAMXXRGIRPVGR 19

DB 217 PYTEPFTALRGLELLGR 234

Best Local Similarity	46.28;	Pred. No. 17;			
Matches	6; Conservative	2; Mismatches	5; Indels	0; Gaps	0;

```
Qy      2 PDINPAWYXXRGI 14
          | : | | | :
Db      40 PPMNPLWYSILGV 52
```

RESULT 12

opsin, lateral eye - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C:Accession: B48197
R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Batteille, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A:Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus
A:Reference number: A48197; M01D:93317641
A:Accession: B48197
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-376 <SMI>
A:Cross-references: EMBL:L03791; NID:9156642; PID:AAA28273.1; PID:9156643
C:Superfamily: vertebrate rhodopsin
C:Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; retinal
E:318/Blinding site: retinal (lys) (covalent) #status predicted

Query Match	39.48;	Score 43;	DB 2;	Length 376;
Best Local Similarity	46.28;	Pred. NO. 17;		
Matches	6;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0

```
Qy      2 PDINPAWYXXRGI 14
         | : | | | :
Db      40 PPMNP L WYSILGV 52
```

RESULT 13

probable amino acid transport protein yaaJ, sodium-dependent - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Aug-1999
 C:Accession: G64720
 R:Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
 A.: Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: G64720
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-476 <BLAT>
 A:Cross-references: G8:AE00111, G8:U00096; NID:g1786181; PIDN:ANC73118.1; PID:g17861818;
 A:Experimental source: strain K-12, substrain M6155
 C:Genetics:
 A:Gene: yaaJ
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein
 C:Keywords: amino acid transport; transmembrane protein
 F:10-26/Domain: transmembrane #status predicted <TM1>
 F:91-107/Domain: transmembrane #status predicted <TM2>
 F:142-158/Domain: transmembrane #status predicted <TM3>
 F:178-194/Domain: transmembrane #status predicted <TM4>
 F:208-224/Domain: transmembrane #status predicted <TM5>
 F:303-319/Domain: transmembrane #status predicted <TM6>
 F:349-365/Domain: transmembrane #status predicted <TM7>
 F:391-407/Domain: transmembrane #status predicted <TM8>
 F:414-430/Domain: transmembrane #status predicted <TM9>

Query Match	39.4%	Score 43;	DB 2;	Length 476;
Best Local Similarity	44.4%;	Pred. No. 22;		
Matches -- 8;	Conservative	2;	Mismatches	2;
			Indels	6;
			Gaps	1.

```
QY      3 DIN-----PAWYXXRG I 14
      1:|      ||| 11:
Db     120 DVNGQFRGGPAWYMARG L 13
```

RESULT 14

Arp1 protein yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein D1478; protein YDL167c
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Dec-1999
 C:Accession: S61046, S31139; S67719
 R:Pol1, T.M.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: S61010
 A:Accession: S61046
 A:Molecule type: DNA
 A:Residues: 1-719 <PDB>
 A:Cross-references: EMBL:Z67750; NID:g1061256; PIDD:CAA91579.1; PID:g1061272
 R:Meiner, E.P., Rao, E.; Brendel, M.
 Mol. Gen. Genet. 237, 351-358, 1993
 A:Title: Molecular structure and genetic regulation of Sfr, a gene responsible for re
 A:Reference number: S31138; MUID:93247548
 A:Accession: S31139
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-492, 'N', 494-719 <MEH>
 A:Cross-references: EMBL:X66020; NID:g577609; PIDD:CAA48159.1; PID:g288590
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R:Pol1, T.M.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67708
 A:Accession: S67719
 A:Molecule type: DNA
 A:Residues: 1-719 <PDB>
 A:Cross-references: EMBL:Z74215; NID:g1431265; PIDD:CAA98741.1; PID:e253076; PID:g143
 C:Experimental source: strain 5288C
 C:Genetics:
 A:Gene: SGD:NRPL; ARP1
 A:Cross-references: MIPS:YDL167c; SGD:S0002326
 A:Map position: 4L

Query Match	39.4%	Score 43	DB 2	Length 719
Best Local	Similarity 50.0%	Pred. No. 33		
Matches	6	Conservative	3	Mismatches 0
				Gaps 0

```
QY      7 AMYXXRGIRPVG 18
          :|: |:|||
Db     244 SWETQYGVPRVG 255
```

RESULT 15

110032
 hypothetical protein T13C2.5 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: T16859
 R:Du, Z.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid T13C2.
 A:Reference number: Z18591
 A:Accession: T16859
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1296 <RDZ>
 A:Cross-references: EMBL:U40030; NID:g1055164; PID:g1055165; PIDN:AAA8133.1; CESP:T1
 C:Genetics:
 A:Gene: CESP:T13C2.5
 A:Introns: 62/3; 93/3; 124/3; 142/1; 212/1; 293/1; 336/2; 406/3; 437/1; 508/1; 584/1;

Best Local Similarity 45.0%; Pred. No. 60;
 Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
 QY 1 TPDINPARYXXRGIRPVGRF 20
 | | | | | : : | |
 Db 975 TTDINSDWTFSR--KDINRF 992

Search completed: April 17, 2001, 15:45:59
 Job time: 607 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2001, 15:48:53 ; Search time 39.1 seconds
(without alignments)
19.274 Million cell updates/sec

Title: US-09-446-543A-73

Perfect score: 109
Sequence: 1 TPDIINPAWYXXRGI RPYGRFX 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	96.3	87	PRRP_HUMAN	P81277 homo sapien
2	104	95.4	83	PRRP_RAT	P81278 rattus norv
3	104	95.4	98	PRRP_BOVIN	P81265 bos taurin
4	46	42.2	676	EXL1_HUMAN	O92935 homo sapien
5	43	39.4	376	OPSL_LIMPO	P35360 limulus pol
6	43	39.4	376	OPSL2_LIMPO	P35361 limulus pol
7	43	39.4	383	CYCR_CHRVI	O82947 chromatiu
8	43	39.4	476	YAAJ_ECOLI	P30143 escherichia
9	43	39.4	719	ARP_YEAST	P32770 saccharomy
10	41	37.6	342	Y762_METUA	O58172 methanococ
11	41	37.6	347	Y576_METUA	O57996 methanococ
12	41	37.6	986	CYGR_ARBPJ	P15288 arpacia pun
13	40	36.7	329	Y493_MYCTU	Q11558 mycobacteri
14	40	36.7	546	CHOD_STRSQ	P12676 streptomyce
15	40	36.7	581	POL_MLYRK	P31795 radiatlon m
16	40	36.7	843	POL_MLYRK	P03357 akt murine
17	40	36.7	1196	POL_MLYRK	P03356 akt murine
18	40	36.7	1196	POL_MLYRK	P11227 radiatlon m
19	39.5	36.2	860	VG12_BPB03	Q37893 bacterioph
20	39	35.8	149	ENRM_BPT7	P00641 bacterioph
21	39	35.8	360	WMT2_HUMAN	P09944 homo sapien
22	39	35.8	377	OPSL1_HEMSA	Q25157 hemigrapsu
23	39	35.8	377	OPSL2_HEMSA	Q25158 hemigrapsu
24	39	35.8	622	OPSC_RAT	P07379 rattus norv
25	39	35.8	953	SVY_VIBCH	Q9K673 vibrlio chol
26	39	35.8	962	UVRA_METTN	O25643 methanobact
27	38.5	35.3	240	PLSC_HELPY	O25603 heliocobact
28	38.5	35.3	265	UBIE_RICPR	Q926P3 rickettsia
29	38.5	35.3	831	DPO1_THIEL	P30133 thermus agu
30	38.5	35.3	877	CAD2_BOVIN	P19934 bos taurin
31	38.5	35.3	906	CAD2_HUMAN	P19922 homo sapien
32	38.5	35.3	906	CAD2_MOUSE	P15116 mus musculu
33	38.5	35.3	3083	POLG_ZYMR	O89330 z genome po

34	38	34.9	158	1	RL15_AERPE	Q9YF98 aeropyrum p
35	38	34.9	197	1	118B_HUMAN	O95998 homo sapien
36	38	34.9	261	1	PHSC_ECOLI	P77409 escherichia
37	38	34.9	332	1	LYTB_MYCLE	Q9X781 mycobacteri
38	38	34.9	399	1	HMPA_BACSU	P49852 bacillus su
39	38	34.9	951	1	SVY_ECOLI	P07118 escherichia
40	38	34.9	994	1	GLNE_MYCTU	Q10379 mycobacteri
41	38	34.9	1723	1	AIM1_HUMAN	Q9Y4K1 homo sapien
42	38	34.9	2870	1	MDVB_RHINE	P20471 rhizobium m
43	37	33.9	179	1	RK6_GUTTH	O46908 guillardi
44	37	33.9	251	1	VP24_EBOG4	O14659 ebola virus
45	37	33.9	251	1	VP24_EBOZM	Q05322 ebola virus

ALIGNMENTS

RESULT 1

PRRP_HUMAN STANDARD: PRT: 87 AA.

AC P81277; 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING DE HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20].
GN PRR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92868781; PubMed=9607765;
RA Huhma S., Habeta Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kikawa C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda N., Fujino M.;
RT "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-276(1998).

-1- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGFR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.
CC -1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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CC
CC EMBL: AB015419; BAA29027.1; -
CC MIM: 602653; -
CC Normone; Amidation: Signal.
CC SIGNAL 1 22
CC FT PEPTIDE 23 53 BY SIMILARITY.
CC FT PEPTIDE 34 53 PROLACTIN-RELEASING PEPTIDE PRRP31.
CC FT MOD.RES 53 53 PROLACTIN (6-54 PROVIDE AMIDE GROUP).
CC AMIDATION (6-54 PROVIDE AMIDE GROUP).
CC SQ SEQUENCE 87 AA; 9639 MW; 229A2F3E50CF981B CRC64;

Query Match Best local Similarity 96.3%; Score 105; DB 1; Length 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDIINPAWYXXRGI RPYGRFX 20
DB 34 TPDIINPAWYXXRGI RPYGRFX 53

```

RESULT 2
PRRP_RAT PRRP_BOVIN STANDARD: PRT: 83 AA.
AC P81278:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING
HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-
RELEASING PEPTIDE PRRP20].
GN PRH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kitada C., Masuo Y., Asano T., Matsunoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Onda H., Fujino M.,
RT "A prolactin-releasing peptide in the brain.";
RA Nature 393:272-276(1998).
CC -1- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE
CC EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE
CC LACTORRHOUS DIRECTLY TO SECRETE PRL.
CC -1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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CC or send an email to license@slb-slb.ch).
CC -----
DR EMBL; AB015418; BAA29026.1; -
KM Hormone; Amidation; Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 21
FT PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31.
FT PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.
FT MOD.RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).
SQ SEQUENCE 83 AA; 9215 MW; DDC75A264EE4F29 CRC64;
Query Match 95.4%; Score 104; DB 1; Length 83;
Best Local Similarity 90.0%; Pct. No. 2e-10; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TPDIHPAWYXXGIRPVGRF 20
| | | | | | | | | | | | | | | | | | | | | |
DB 33 TPDIHPAWYXXGIRPVGRF 52
RESULT 3
PRRP_BOVIN STANDARD: PRT: 98 AA.
AC P81264:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING
HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-
RELEASING PEPTIDE PRRP20].
GN PRH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.

```

RC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kikuchi C., Masuo Y., Asano T., Matsunoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT "A prolactin-releasing peptide in the brain.";
RT Nature 393:277-276(1998).
CC -1- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE
CC EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR MGR3. MAY STIMULATE
CC LACTOTROPHS DIRECTLY TO SECRETE PRL.
CC -1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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CC or send an email to license@lsb-sib.ch).
CC -----
CC DR EMBL: AB015417; BAA29025.1; -
KM Hormone: Amidation; Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 22
FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRPP31.
FT PEPTIDE 33 53 PROLACTIN-RELEASING PEPTIDE PRPP20.
FT MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
FT MOD_RES 53 53
SO SEQUENCE 98 AA; 10544 MW; 08AC35A13B0FA908 CRC64;

Query Match 95.4%; Score 104; DB 1; length 98;
Best Local Similarity 90.0%; Pred. No. 2.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPDIINPAWYXXNGIRPVGRF 20
||||||| |||||
DB 34 TPDIINPAWYAGRGIRPVGRF 53

RESULT 4
ID EX1L_HUMAN STANDARD: PRT; 676 AA.
AC 092935;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EXOSTOSIN-Like 1 (EXOSTOSIN-L) (MULTIPLE EXOSTOSIS-LIKE PROTEIN).
GN EX1L OR EXTL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97189339; PubMed=9037597;
RA Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.;
RT "Identification and localization of the gene for EXTL, a third member
RT of the multiple exostoses gene family.";
RL Genome Res. 7:10-16(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L., Deng H.X., Xia J.H., Pan Q., Liu C.Y.;
RT "Mutations of the EXT genes in hereditary multiple exostoses in
RT Chinese.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wuyts W., Speker N., Van Roy N., De Paeppe A., De Boulle K.,
RA Williams P.J., Van Hul W., Versteeg R., Speleman F.;
RT "Refined physical mapping and genomic structure of the EXTL1 gene.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC
CC RETICULUM (BY SIMILARITY).
CC -----

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CC -1- SIMILARITY: BELONGS TO THE EXOSOMIN FAMILY
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; U67191; AAC51141.1; -.
DR EMBL; AF083633; AAD02840.1; JOINED.
DR EMBL; AF083623; AAD02840.1; JOINED.
DR EMBL; AF083624; AAD02840.1; JOINED.
DR EMBL; AF083625; AAD02840.1; JOINED.
DR EMBL; AF083626; AAD02840.1; JOINED.
DR EMBL; AF083627; AAD02840.1; JOINED.
DR EMBL; AF083628; AAD02840.1; JOINED.
DR EMBL; AF083629; AAD02840.1; JOINED.
DR EMBL; AF083630; AAD02840.1; JOINED.
DR EMBL; AF083631; AAD02840.1; JOINED.
DR EMBL; AF083632; AAD02840.1; JOINED.
DR EMBL; AF153980; AAF73172.1; -.
DR EMBL; AF151391; AAF73172.1; JOINED.
DR MM; 601738; -.
KW Anticoccogene; Multigene family; Transmembrane; signal-anchor.
FT TRANSMEM 10 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
PT N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 676 AA; 74673 MW; B5E06A8762E5633 CRC64;.
OY 1 TPDIHPANYXXRGIPVGRF 20
Db 400 SPODFPYTLDOGSREGRF 419
RESULT 5
OPSL_LIMPO STANDARD; PRT; 376 AA.
AC P33360;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE LATERAL EYE OPSIN.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OX Limulidae; Limulus.
CX NCBI_TaxID=6850; [1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Lateral eye;
RA MEDLINE=93317641; Pubmed=8327495;
RT Smith W.C., Price D.A., Greenberg R.M., Battelle B.-A.;
RT "Opsins from the lateral eyes and ocelli of the horseshoe crab,
RT Limulus polyphemus." ;
RL Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).
CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: LATERAL EYE.
CC -1- PM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMA AT 520 NM.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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RL Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).
 CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
 CC MEDIANE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
 CC LINKED TO CIS-RETINAL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: OCULAR CELLS; MEDIAN OCELLI.
 CC -1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
 CC BE PHOSPHORYLATED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMA AT 530 NM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC OPSIN SUBFAMILY.
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 CC -----
 CC DR EMBL: L03792; AAA28274.1; -
 CC DR EMBL: L03782; AAA02499.1; -
 CC DR PIR: A48197; A48197.
 CC GCRDB: GCR_0585; -
 CC DR InterPro: IPR000276; -
 CC DR InterPro: IPR001591; -
 CC DR InterPro: IPR001760; -
 CC Pfam: PF00001; 7cm.1; 1.
 CC DR PRINTS: PR00237; GPCRHHODPSN.
 CC DR PRINTS: PR00238; OPSIN.
 CC DR PRINTS: PR00578; OPSINTRLEYE.
 CC DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; I.
 CC DR PROSITE: PS00262; G_PROTEIN_RECIP_F1_2; I.
 CC DR PROSITE: PS00238; OPSIN; 1.
 CC DR KMW Phosphorylation: Retinal protein; Transmembrane; Glycoprotein; Vision;
 CC KMW Phosphorylation: G-protein coupled receptor.
 CC FT DOMAIN 1 46
 CC FT TRANSMEM 47 71
 CC FT TRANSMEM 72 83
 CC FT TRANSMEM 84 108
 CC FT TRANSMEM 109 123
 CC FT TRANSMEM 124 143
 CC FT TRANSMEM 144 162
 CC FT TRANSMEM 163 186
 CC FT TRANSMEM 187 210
 CC FT TRANSMEM 211 238
 CC FT TRANSMEM 239 274
 CC FT TRANSMEM 275 298
 CC FT TRANSMEM 299 306
 CC FT TRANSMEM 307 331
 CC FT TRANSMEM 332 376
 CC FT DISULFID 120 197
 CC FT BINDING 318 318
 CC FT CARBOHYD 17 17
 CC FT CARBOHYD 193 193
 CC FT SEQUENCE 376 AA; 42111 MW; FA9647C4D531CBF8 CRC64;
 SQ
 Query Match 39.4%; Score 43; DB 1; Length 376;
 Best Local Similarity 46.2%; Pred. No. 8.5;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT PRECURSOR.
 GN PUF.
 OS Chromatium vinosum.
 CC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
 CC Allochrocatium.
 CC NCBI_TaxID=1049;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-D:
 CC Corson G.E., Nagashima K.V., Matsura K., Sakurai Y., Ruvantni W.,
 CC Qin H., Allen R., Knaf D.B.:
 CC "Primary structure of genes encoding light-harvesting and reaction
 CC center proteins from Chromatium vinosum."
 CC Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A
 CC TIGHTLY BOUND CYTOCHROME MOLECULE WHICH REDUCES THE PHOTO
 CC OXIDIZED PRIMARY ELECTRON DONOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
 CC ANCHOR (BY SIMILARITY).
 CC -1- PTM: BINDS FOUR HEME GROUPS PER MOLECULE.
 CC -1- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER
 CC CYTOCHROME C SUBUNITS.
 CC -----
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 CC -----
 CC DR EMBL: AB011811; BAA32742.1; -
 CC DR InterPro: IPR000345; -
 CC DR PROSITE: PS00190; CYTOCHROME_C_4.
 CC DR KMW Electron transport: Photosynthesis; Reaction center; Heme;
 CC KMW Membrane: Lipoprotein; Duplication; Signal.
 CC KMW SIGNAL 1 22
 CC KMW CHAIN 23 383
 CC FT LIPID 23 23
 CC FT BINDING 107 107
 CC FT BINDING 110 110
 CC FT BINDING 111 111
 CC FT METAL 152 152
 CC FT BINDING 153 155
 CC FT BINDING 156 156
 CC FT METAL 247 247
 CC FT BINDING 250 250
 CC FT METAL 251 251
 CC FT BINDING 307 307
 CC FT BINDING 310 310
 CC FT METAL 311 311
 CC FT SEQUENCE 383 AA; 41522 MW; 96BCD91F1B9AE7E CRC64;
 SQ
 Query Match 39.4%; Score 43; DB 1; Length 383;
 Best Local Similarity 36.8%; Pred. No. 8.6;
 Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;


```

GN MJ0762.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus
OC NCBI_TaxID=2150;
RX
  RP SEQUENCE FROM N.A.
  RX STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
  RX MEOLINE-96337999; PubMed-8688087;
  RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.O.,
  RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.O.,
  RA Kierulff A.R., Dougherty B.A., Tomb J.-F., Adams M.O., Reich C.I.,
  RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
  RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen O.,
  RA Ullrich J., Kelley J.M., Peterson J.O., Sadow P.W., Hanna M.C.,
  RA Cotton M.O., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
  RA Klenk N.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
  RA Complete genome sequence of the methanogenic archaeon, Methanococcus
  RA jannaschii.
  RT Science 273:1058-1073(1996).
  CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
  CC -1- SIMILARITY: SPRONG, TO M.JANNASCHII MJ0762 AND TO S.POMBE MALATE
  CC PERLEASE (MAEL).
  CC -----
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  CC -----
  OR EMBL: U67521; AAB98753.1; -.
  DR TIGR: MJ0762; -.
  KW Hypothetical protein; Transmembrane; Transport.
  FT TRANSMEM 8
  FT TRANSMEM 28
  FT TRANSMEM 39
  FT TRANSMEM 59
  FT TRANSMEM 79
  FT TRANSMEM 99
  FT TRANSMEM 108
  FT TRANSMEM 128
  FT TRANSMEM 142
  FT TRANSMEM 162
  FT TRANSMEM 175
  FT TRANSMEM 195
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  FT TRANSMEM 227
  FT TRANSMEM 242
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  FT TRANSMEM 1189
  FT TRANSMEM 1200
  FT TRANSMEM 1211
  FT TRANSMEM 1222
  FT TRANSMEM 1233
  FT TRANSMEM 1244
  FT TRANSMEM 1255
  FT TRANSMEM 1266
  FT TRANSMEM 1277
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  FT TRANSMEM 12321
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  FT TRANSMEM 12486
  FT TRANSMEM 12497
  FT TRANSMEM 12508
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  FT TRANSMEM 12574
  FT TRANSMEM 12585
  FT TRANSMEM 12596
  FT TRANSMEM 12607
  FT TRANSMEM 12618
  FT TRANSMEM 12629
  FT TRANSMEM 12640
  FT TRANS
```

CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-CYCLIC GMP + PYROPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC
 CC DOMAIN OF PROTEIN KINASES.
 CC
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 CC
 CC EMBL: X12874; CAA31367.1; -
 CC PIR: S05480; OYRGA.
 CC InterPro: IPR001828; -
 CC InterPro: IPR001828; -
 CC Pfam: PF01094; ANF_receptor; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Receptor: Transmembrane; Glycoprotein; Phosphorylation; Lyase;
 CC GMP synthetase; Signal.
 CC
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 966
 CC FT DOMAIN 22 507
 CC FT TRANSMEM 508 528
 CC FT DOMAIN 529 986
 CC FT DOMAIN 568 836
 CC FT CARBOHYD 185 185
 CC FT CARBOHYD 361 361
 CC FT CARBOHYD 410 410
 CC SEQUENCE 986 AA; 111284 MW; B40238A74CCARC52 CRC64;
 SO
 OY 2 PDINPAMY 9
 Db 475 PDINPAMY 482
 Query Match 37.6%; Score 41; DB 1; Length 986;
 Best Local Similarity 62.5%; Pred. No. 46;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 RESULT 13
 Y493_MYCTU STANDARD; PRT; 329 AA.
 AC 011158;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOHETICAL 35.4 KDA PROTEIN RY0493C.
 GN RY0493C OR MYCY2069.19C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1773;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE:98295987; PubMed:9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla E.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLaren J., Moule S., Murphy L.,
 RA Oliver S., Osondo J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutherford S., Seeger K., Skellern S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC -1- SIMILARITY: SOME, TO M. LEPRAE B2168_F2_93.
 CC

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 CC
 CC EMBL: Z77162; CAB00954.1; -
 CC DR Tuberculosis; RY0493C; -
 CC DR Hypothetical protein.
 CC SEQUENCE 329 AA; 35427 MW; BE4B524750277B56 CRC64;
 SO
 OY 2 PDINPAMYXRGIR 15
 Db 90 PDINPAMYXRGIR 103
 Query Match 36.7%; Score 40; DB 1; Length 329;
 Best Local Similarity 42.9%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 RESULT 14
 CHOD_STRSQ STANDARD; PRT; 546 AA.
 ID CHOD_STRSQ
 AC P12676;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CHOLESTEROL OXIDASE PRECURSOR (EC 1.1.3.6) (CHOD).
 GN CHOA.
 OS Streptomyces sp. (strain SA-COO).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetes.
 OX NCBI_Taxid=1931;
 RN 11)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89123081; PubMed-2914856;
 RA Ishizaki T., Hirayama N., Shinkawa H., Nimi O., Murooka Y.;
 RT Nucleotide sequence of the gene for cholesterol oxidase from a
 RT Streptomyces sp.";
 RL J. Bacteriol. 171:596-601(1989).
 RN 12)
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE-99211873; PubMed-10194345; Vrieland A.;
 RA Yue Q.K., Kass I.J., Sampson N.S., Vrieland A.;
 RT "Crystal structure determination of cholesterol oxidase from
 RT Streptomyces and structural characterization of key active site
 RT mutants.";
 RL Biochemistry 38:4277-4286(1999).
 CC -1- CATALYTIC ACTIVITY: CHOLESTEROL + O(2) -> CHOLEST-4-EN-3-ONE +
 CC H(2)O(2).
 CC -1- COFACTOR: FAD.
 CC -1- PATHWAY: CHOLESTEROL METABOLISM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
 CC
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 CC
 CC EMBL: M31939; AAA26719.1; -
 CC PIR: A33260; A33260.
 CC DR PDB: 1B4V; 06-JAN-99.
 CC DR PDB: 1B8S; 09-FEB-99.
 CC DR PDB: 1C80; 10-MAR-99.
 CC DR PDB: 1CC2; 11-MAR-99.

DR InterPro: IPR000172; -
 DR InterPro: IPR001167; -
 DR Pfam: PF01319; CHOD; 1.
 DR PROSITE: PS00623; GMC_OXRED_1; 1.
 DR PROSITE: PS00624; GMC_OXRED_2; FALSE_NEG.
 KW Oxidoreductase; Signal; Flavoprotein; FAD; 3D-structure.
 FT SIGNAL 1 42
 FT CHAIN 43 546
 FT NP_BIND 54 70 CHOLESTEROL OXIDASE.
 FT ACT_SITE 398 398 FAD (ADP PART) (POTENTIAL).
 FT ACT_SITE 484 484 PROTON ACCEPTOR.
 FT MOTAGEN 398 398
 FT MOTAGEN 484 484 E->O: REDUCED ACTIVITY.
 FT MOTAGEN 484 484 H->N,O: REDUCED ACTIVITY.
 SQ SEQUENCE 546 AA: 58993 MW: EF22A1P5EA68D21 CRC64;

Query Match 36.7%; Score 40; DB 1: Length 546;
 Best Local Similarity 36.8%; Pred. No. 38;
 Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 2 PDINPAWYXXRGIRPVGRF 20
 DB 98 PDKRSSWPKNRTAPLGSF 116

RESULT IS

POL_MLVK STANDARD: PRT: 581 AA.
 AC P31795;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE POLYPROTEIN (CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE
 TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) (FRAGMENT).
 GN POL.
 OS Radiation murine leukemia virus (strain Kaplan).
 OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
 OX NCBI_TaxID=31689;
 RN [1]
 RP SEQUENCE FROM R.A.
 RX MEDLINE=92333703; PubMed=1629969;
 RA Poliquin L., Bergeron D., Fortier J.L., Paquette Y., Bergeron R.,
 RA Rassart E.;
 RT "Determinants of thymotriplem in Kaplan radiation leukemia virus and
 RT nucleotide sequence of its envelope region";
 RL J. Virol. 66:5141-5146(1992).
 CC -1- PPM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-POL
 CC POLYPROTEIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE
 CC RETROPEPSIN FAMILY.
 CC
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 CC
 CC EMBL: M93052; AAA6525.1; -
 DR PIR: A42743; A42743.
 DR MEROPS: A02.008; -
 DR InterPro: IPR001037; -
 DR InterPro: IPR001584; -
 DR InterPro: IPR001969; -
 DR InterPro: IPR002156; -
 DR Pfam: PF00552; Integrase; 1.
 DR Pfam: PF00075; rnsah; 1.
 DR Pfam: PF00665; rve; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; PARTIAL.
 DR Hydrolase; Transferase; RNA-directed DNA polymerase;
 KW Aspartyl protease; Endonuclease; Polypeptide.

FT NON_TER 1 1
 SQ SEQUENCE 581 AA: 65157 MW: 8D7A38694C8E036E CRC64;

Query Match 36.7%; Score 40; DB 1: Length 581;
 Best Local Similarity 41.2%; Pred. No. 40;
 Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 TPIDNPAWYXXRGIRPV 17
 DB 556 TPPIRPSWYQNSQNP 572

Search completed: April 17, 2001, 15:48:53
 Job time: 541 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2001, 15:48:13 ; Search time 115.07 seconds
(without alignments)
22.409 Million cell updates/sec

Title: US-09-446-543a-73
Perfect score: 109
Sequence: 1 TPDINPAMYXXRGIRPVGRFX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-REMBL-15:*
2: sp-archaea:*
3: sp-bacteria:*
4: sp-fungi:*
5: sp-human:*
6: sp-invertebrate:*
7: sp-mammal:*
8: sp-mmc:*
9: sp-organella:*
10: sp-plant:*
11: sp-rodent:*
12: sp-unclassified:*
13: sp-vertebrate:*
14: sp-virus:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	75.2	117	13 Q9W624	Q9W624 carassius a
2	49	45.0	790	10 Q9M371	Q9M371 arabidopsis
3	46	42.2	54	4 Q9UJF9	Q9UJF9 homo sapien
4	46	42.2	333	2 Q9PH76	Q9PH76 xyella fas
5	46	42.2	463	4 Q60687	Q60687 homo sapien
6	46	42.2	540	10 Q9LG20	Q9LG20 oryza sativ
7	45	41.3	767	5 Q20170	Q20170 caenorhabd
8	44	40.4	284	1 Q50128	Q50128 pyrococcus
9	44	40.4	419	4 Q9Y276	Q9Y276 homo sapien
10	43.5	39.9	1501	10 Q9SD86	Q9SD86 arabidopsis
11	43	39.4	232	2 Q9RZ21	Q9RZ21 deinococcus
12	43	39.4	309	5 Q17234	Q17234 caenorhabd
13	43	39.4	1296	5 Q22452	Q22452 caenorhabd
14	42.5	39.0	333	2 Q9R370	Q9R370 streptomyce
15	42.5	39.0	443	5 Q19879	Q19879 caenorhabd
16	42	38.5	293	2 Q53855	Q53855 spiroplasma
17	42	38.5	428	2 Q9PK87	Q9PK87 chlamydia m
18	41.5	38.1	345	2 Q9K8V2	Q9K8V2 bacillus ha
19	41	37.6	97	2 Q33440	Q33440 pseudomonas

20	41	37.6	128	2 P74747	P74747 synecocyst
21	41	37.6	284	1 Q9V0Q3	Q9V0Q3 pyrococcus
22	41	37.6	328	4 Q9NV85	Q9NV85 homo sapien
23	41	37.6	338	5 Q18729	Q18729 caenorhabd
24	41	37.6	343	2 Q9Z430	Q9Z430 streptomyce
25	41	37.6	414	2 Q33480	Q33480 propionibac
26	41	37.6	547	2 Q55020	Q55020 streptomyce
27	41	37.6	2155	11 Q08523	Q08523 mus musculu
28	40.5	37.2	779	3 Q9P5J9	Q9P5J9 neurospora
29	40.5	37.2	1540	10 Q9SD90	Q9SD90 arabidopsis
30	40	36.7	76	5 Q9V8L0	Q9V8L0 drosophila
31	40	36.7	153	3 Q9T133	Q9T133 bacterioph
32	40	36.7	181	3 Q9USE8	Q9USE8 schizosacch
33	40	36.7	184	2 Q86838	Q86838 streptomyce
34	40	36.7	207	5 Q27455	Q27455 brachycentr
35	40	36.7	213	5 Q9VHT8	Q9VHT8 drosophila
36	40	36.7	244	10 Q9SD09	Q9SD09 arabidopsis
37	40	36.7	324	2 Q9Z554	Q9Z554 streptomyce
38	40	36.7	341	2 Q9X7Y1	Q9X7Y1 streptomyce
39	40	36.7	359	3 Q59676	Q59676 schizosacch
40	40	36.7	390	2 Q9PH18	Q9PH18 xyella fas
41	40	36.7	402	2 Q9KIW3	Q9KIW3 chloobacillu
42	40	36.7	430	1 Q27142	Q27142 methanobact
43	40	36.7	462	10 Q39249	Q39249 arabidopsis
44	40	36.7	466	2 Q54042	Q54042 pseudomonas
45	40	36.7	562	5 Q9VN94	Q9VN94 drosophila

ALIGNMENTS

RESULT 1
ID Q9W624 PRELIMINARY: PRT: 117 AA.
AC Q9W624:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C-RF AMIDE PRECURSOR
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OX Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RA Satake H., Minakata H., Fujimoto M.;
RL "Carassius Rfamidae (C-RF amide).";
DR EMBL: AB020024; DAA76662.1; -
SQ SUBMITTED (NOV-1998) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;

Query Match 75.2% Score 82; DB 13; Length 117;
Best Local Similarity 60.0% Pred. No. 3.3e-06;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TPDINPAMYXXRGIRPVGRF 20
Db 56 SPEIDPFMTVGRVPRIGRF 75
RESULT 2
ID Q9M371 PRELIMINARY: PRT: 790 AA.
AC Q9M371:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 87.4 KDA PROTEIN.
GN F15G16.60.
OS Arabidopsis thaliana (Mouse-ear cress).

Best Local Similarity 43.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 TPDINPAMYXXRGIRP 16
11:111111
DB 18 TPVATPTWYAGSGYYP 33

RESULT 6
O9LGZ0

ID 09LGZ0 PRELIMINARY; PRT; 540 AA.

AC 09LGZ0;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE EST AU070209(83722) CORRESPONDS TO A REGION OF THE PREDICTED GENE.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

OX NCBI_Taxid=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT *Oryza sativa nippobare(GAS) genomic DNA, chromosome 1, PAC

RT clone:PO702F03.;

RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AP000481; BAA9583.1; -; SDE1F4EEB75A86E CRC64;

SO SEQUENCE 540 AA; 60487 MW; 5DE1F4EEB75A86E CRC64;

Query Match 42.2%; Score 46; DB 10; Length 540;

Best Local Similarity 50.0%; Pred. No. 15;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 DINPAMYXXRGIRP 16
11:111111
DB 69 DLGVAMWVRGLRP 82

RESULT 7
O20170
AC 020170; PRELIMINARY; PRT; 767 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE F38E11.7.

GN F38E11.7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Psolodierinae; Caenorhabditis.

OX NCBI_Taxid=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Matthews P.;

RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE-94150718; PubMed-7906398;

RA Wilson R., Almscough R., Anderson R., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,

RA *2.2 kb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.;

RL Nature 368:32-38(1994).

DR EMBL: Z68342; CAA92775.1; -;

DR INTERPRO: IPR000595; -;

DR INTERPRO: IPR001622; -;

DR INTERPRO: IPR002025; -;

DR PFAM: PF00027; CIMP_binding; 1.

DR PFAM: PF00914; CIMP_binding; 1.

DR PROSITE: PS00888; CIMP_BINDING_1; UNKNOWN_1.

DR PROSITE: PS00442; CIMP_BINDING_3; 1.

SO SEQUENCE 767 AA; 89988 MW; F7ECF69DBBBAACF3 CRC64;

Query Match 41.3%; Score 45; DB 5; Length 767;

Best Local Similarity 75.0%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PDINPAMY 9
11:111111
DB 747 PDVCPAMY 754

RESULT 8
O50128

ID O50128 PRELIMINARY; PRT; 284 AA.

AC O50128;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE HYPOTHETICAL 32.3 KDA PROTEIN PH1420.

GN PH1420.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.

OX NCBI_Taxid=53953;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OT3;

RA MEDLINE-98344137; PubMed-9679194;

RA Kwarababayasi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,

RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kusuda N., Oguchi A.,

RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

RA Masukhi Y., Shizuya H., Kikuchi H.;

RT Complete sequence and gene organization of the genome of a hyper-

thermophilic archaeobacterium, Pyrococcus horikoshii OT3.;

RL DNA Res. 5:55-76(1998).

DR EMBL: AP000006; BAA30526.1; -;

DR INTERPRO: IPR001066; -;

DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.

KW Hypothetical protein.

SO SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3815 CRC64;

Query Match 40.4%; Score 44; DB 1; Length 284;

Best Local Similarity 44.4%; Pred. No. 17;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 PDINPAMYXXRGIRPVOR 19
11:111111
DB 217 PYLEPTFYALRGLELLGR 234

RESULT 9
O9Y276

ID O9Y276 PRELIMINARY; PRT; 419 AA.

AC O9Y276;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE H-BCS1.

GN BCS1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99097350; PubMed=9878253;
 RA Petruzzella V., Tiranti V., Fernandez P., Ianna P., Carozzo R.,
 Zeviani M.;
 RT Identification and characterization of human cDNAs specific to BCS1,
 PEP112, SCO1, COX15, and COX11, five genes involved in the formation
 of and function of the mitochondrial respiratory chain.;
 RL Genomics 54:494-504(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=96307227; PubMed=8619474;
 RA Andersson B., Wentland M.A., Ricalfente J.Y., Liu W., Gibbs R.A.;
 RT "A double adaptor" method for improved shotgun library
 construction.;
 RL Anal. Biochem. 236:107-113(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Morley K.C., Muzny D.M., Ding Y., Liu W.,
 Ricalfente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT Large-scale concatenation cDNA sequencing.;
 RL Genome Res. 7:353-358(1997).
 DR EMBL: AF026849; AAD08638.1;
 DR EMBL: AF038195; AAB97365.1;
 DR INTERPRO: IPR001939;
 DR PFM: PF00004; AAA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 419 AA; 47534 MW; 7F0F9BBA62P2CB8 CRC64;

Query Match 40.4%; Score 44; DB 4; Length 419;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 NPAMYXXRG1 14
 DB 211 NPKMYTDRG1 220

RESULT 10
 O9SD86 PRELIMINARY; PRT: 1501 AA.
 AC O9SD86;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE HYPOTHEICAL 164.4 KDA PROTEIN.
 GN FLJG24.180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 GN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
 Volckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL133421; CAB62610.1;
 KW Hypothetical protein.
 SQ SEQUENCE 1501 AA; 164360 MW; EAD2AE0C9EBE5D2 CRC64;

Query Match 39.9%; Score 43.5; DB 10; Length 1501;

Best Local Similarity 34.5%; Pred. No. 1.2e+02;
 Matches 10; Conservative 5; Mismatches 5; Indels 9; Gaps 2;
 OY 1 TPDPINAWYXXRG-----LRPV---GRF 20
 DB 1184 SPQMAPSWISQYTFKNGLVQVPYNDIGRF 1212

RESULT 11
 O9R221 PRELIMINARY; PRT: 232 AA.
 AC O9R221;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TEMBLrel. 14, Last annotation update)
 DE HYPOTHEICAL 25.0 KDA PROTEIN.
 GN DRA0132.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_Taxid=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RL;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischman R.D.,
 RA Kelchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome Sequence of the Radioresistant Bacterium Deinococcus
 radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AB001862; AAF12317.1;
 DR TIGR: DRA0132;
 KW Hypothetical protein.
 SQ SEQUENCE 232 AA; 24979 MW; A044FA2E38435DA7 CRC64;

Query Match 39.4%; Score 43; DB 2; Length 232;
 Best Local Similarity 46.7%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 PDIPNAYXXRG1P 16
 DB 130 PDHRAAHLLRGVLP 144

RESULT 12
 O17234 PRELIMINARY; PRT: 309 AA.
 AC O17234;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE 01-JAN-2000 (TEMBLrel. 13, Last annotation update)
 DE K10F12.4 PROTEIN.
 GN K10F12.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 GN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Barks M.,
 RA Bonfield J., Burton J., Connell M., Copsay T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopre A., Saunders D., Showkeen R.,

RA Smaiden N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans*;
 RL Nature 368:32-38(1994).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RA Woldman P., Beck C.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RA Waterston R.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF025462; AAB71002.1; -;
 DR INTERPRO: IPR000521; -;
 DR PFMW: PFD0043; GST; 1.
 DR SEQUENCE 309 AA; 35021 MW; FA2091931D8AD2DC CRC64;
 SQ

Query Match 39.4%; Score 43; DB 5; Length 309;
 Best Local Similarity 44.4%; Pred. No. 27;
 Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
 Oy 2 PDINPAMYXXRGIRPVGR I9
 ||| ||| : |||
 Db I31 PDRSPMWTLPKS--PIGR 146

RESULT 13

ID 022452 PRELIMINARY: PRT; 1296 AA.
 AC 022452;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE SIMILAR TO AGRIN AND FOLLISTATIN.
 GN TIC32.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Pseudocercariae; Caenorhabditis.
 DX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE-94150718; PubMed=7906398;
 RA Wilson R., Anscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
 RA Smaiden N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans*;
 RL Nature 368:32-38(1994).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Du Z.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U40030; AAB1133.1; -;
 DR HSSP: P37109; 1PCE.
 DR INTERPRO: IPR000561; -;
 DR INTERPRO: IPR001239; -;
 DR INTERPRO: IPR001791; -;
 OR

DR INTERPRO: IPR002049; -;
 DR INTERPRO: IPR002350; -;
 DR PFMW: PFD00503; kazal; 9.
 DR PFMW: PFD0053; laminin_EGF; 2.
 DR PFMW: PFD0054; laminin_G; 1.
 DR PRINTS: PR00290; KAZALINBTR.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
 DR PROSITE: PS0186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 1.
 DR SEQUENCE 1296 AA; 145178 MW; 05094BC185839690 CRC64;
 SQ

Query Match 39.4%; Score 43; DB 5; Length 1296;
 Best Local Similarity 45.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
 Oy 1 TPDINPAMYXXRGIRPVGRF 20
 ||| ||| : |||
 Db 975 TPDINSDWYFSR--KDIRNF 992

RESULT 14

ID 09RJ10 PRELIMINARY: PRT; 333 AA.
 AC 09RJ10;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE NYOTHECTICAL 36.3 KDA PROTEIN.
 GN SCF73.06C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Parhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Redenbach M., Kleser H.M., Denapate D., Elchner A., Cullum J.,
 RA Kinsht N., Hopwood D.A.;
 RT *A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome*;
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: M121746; CAB57411.1; -;
 DR Hypothetical protein.
 DR SEQUENCE 333 AA; 36312 MW; 884FF2861837FD76 CRC64;
 SQ

Query Match 39.0%; Score 42.5; DB 2; Length 333;
 Best Local Similarity 32.3%; Pred. No. 35;
 Matches 10; Conservative 2; Mismatches 8; Indels 11; Gaps 1;
 Oy 1 TPDINPAMYXXRGIRPVGRF 20
 ||| ||| : |||
 Db 19 TPDEPAMRTAIGWTEARLAHGLNPTGRW 49

RESULT 15

ID 019879 PRELIMINARY: PRT; 443 AA.
 AC 019879;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 OR

DE F28D1.8 PROTEIN.
 GN F28D1.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Baynes C.;
 RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94150718; Pubmed-7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershav J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Watson A., Weinstock L., Wilkinson-Spoet J., Woldman P., III of C.
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.
 RL Nature 368:32-38(1994).
 DR EMBL; 270684; CAA94603.1;
 SQ SEQUENCE 443 AA; 48865 MW; D9137BACCCE575E CRC64;

Query Match 39.0%; Score 42.5; DB 5; Length 443;
 Best Local Similarity 37.5%; Pred. No. 47;
 Matches 9; Conservative 3; Mismatches 3; Indels 9; Gaps 1;
 OY 4 INPARYXXR-----GIRPVG 18
 DB 53 INPSMFDWRVSVSIDGHLGIMPIG 76

Search completed: April 17, 2001, 15:48:13
 Job time: 566 sec